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Past cyanobacteria biodiversity in herbarium collections: a time travel to a lost world?

A. Wilmotte [1], I.S. Pessi [1,2], D. Velazquez [1,3], B. Durieu[1], H.D. Laughinghouse[1,4],

[1]InBios – Centre for Protein Engineering, University of Liège, Belgium; [2]Arctic Microbial Ecology Groupe & HELSUS, University of Helsinki, Finland; [3]Department of Biology, Universidad Autonoma de Madrid, Spain; [4]Agronomy Department, Ft. Lauderdale Research and Education Center, University of Florida - IFAS, Florida, USA

Email of presenting author: awilmotte@uliege.be

A pilot study of the cyanobacterial diversity in ten herbarium samples from the Smithsonian Institution (Washington DC, USA) was carried out. The samples had been collected between 1897 and 1964 in Antarctica, Alaska, Yellowstone Park and Austrian and American glaciers. The V3-V4 portion of the 16S rRNA gene was sequenced by multiplex 454 pyrosequencing and data was analyzed using the bioinformatic pipeline of Pessi et al. (2016). We obtained 131 OTUs (threshold of 97.5% 16S rRNA similarity), of which 74 were very closely related to existing sequences in public databases. Moreover, the diversity patterns were different between samples, ruling out an homogenization due to contaminations during the handling of herbarium samples since their collection and in our laboratory.

The older specimen (1898) came from a pool at 46°C in Yellowstone Park with dominant sequences of *Stigonema* and *Leptolyngbya*, that are known from these biotopes. For the Antarctic samples taken in 1948-9 from Ross Island, in 1940 from Deception Island and in 1964 from Victoria Land, the DNA could be amplified in all cases and 55 OTUs were detected. Sequences of *Nostoc sp.*, *Microcoleus sp.*, *Phormidesmis priestleyi*, *Leptolyngbya sp*., and *Timaviella sp*. were retrieved. An Alaskan river specimen from 1949 yielded mostly *Nostoc* sequences, as could be expected from the herbarium label. This study gives access to the cyanobacterial community composition in a period where anthropogenic and climatic pressures were still low in the remote polar regions. We will assess if it is possible to detect changes in biogeographic patterns or shifts of genotypes towards more generalist ones.

Pessi, S.I., De Carvalho Maalouf, P., Laughinghouse, H. D., Baurain, D., & Wilmotte, A. (2016). On the use of High-Throughput Sequencing for the study of cyanobacterial diversity in Antarctic aquatic mats. Journal of Phycology, 52, 356–368.